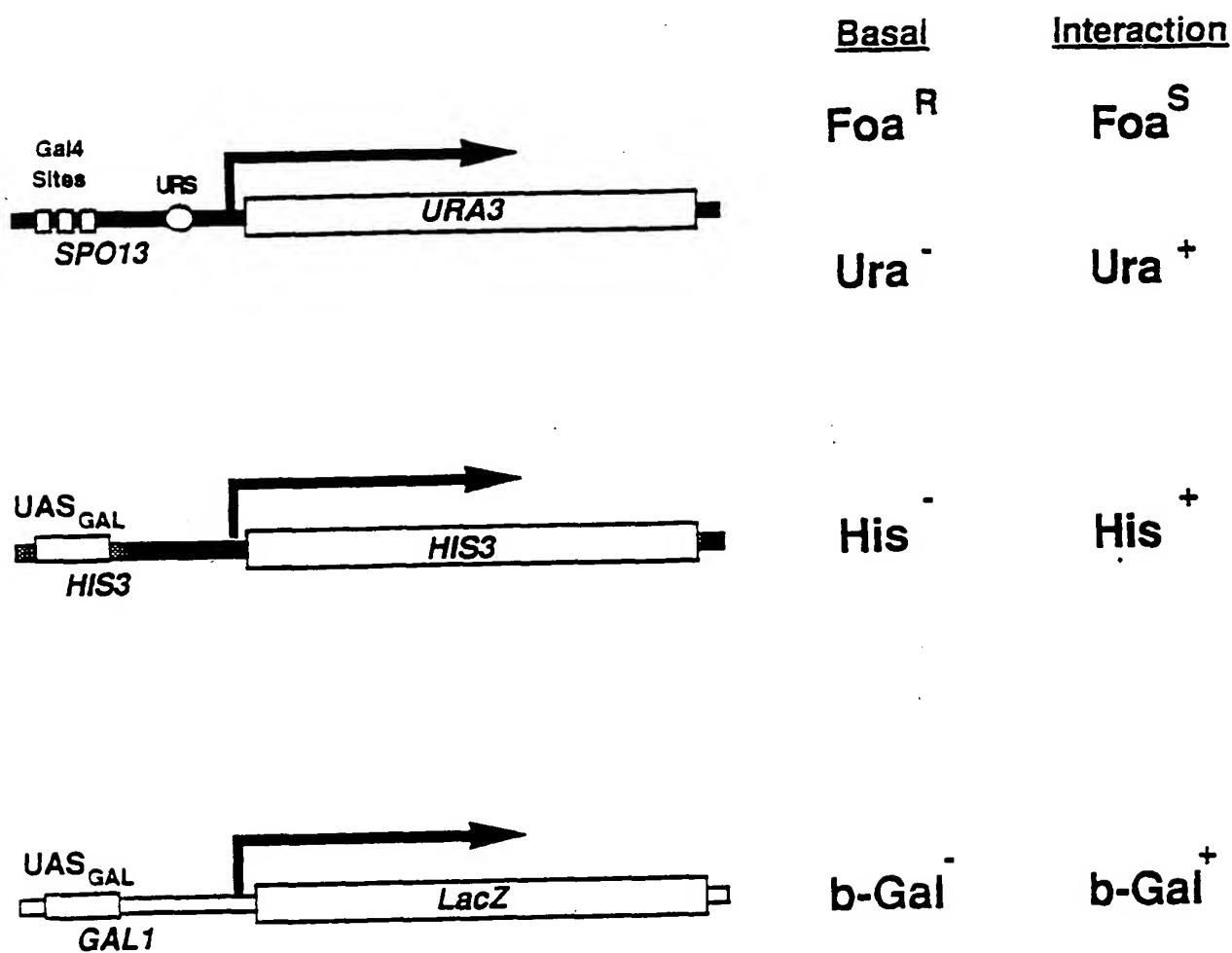


FIGURE 1

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 Applicant(s): Marc Vidal et al.
 REVERSE TWO-HYBRID SYSTEMS

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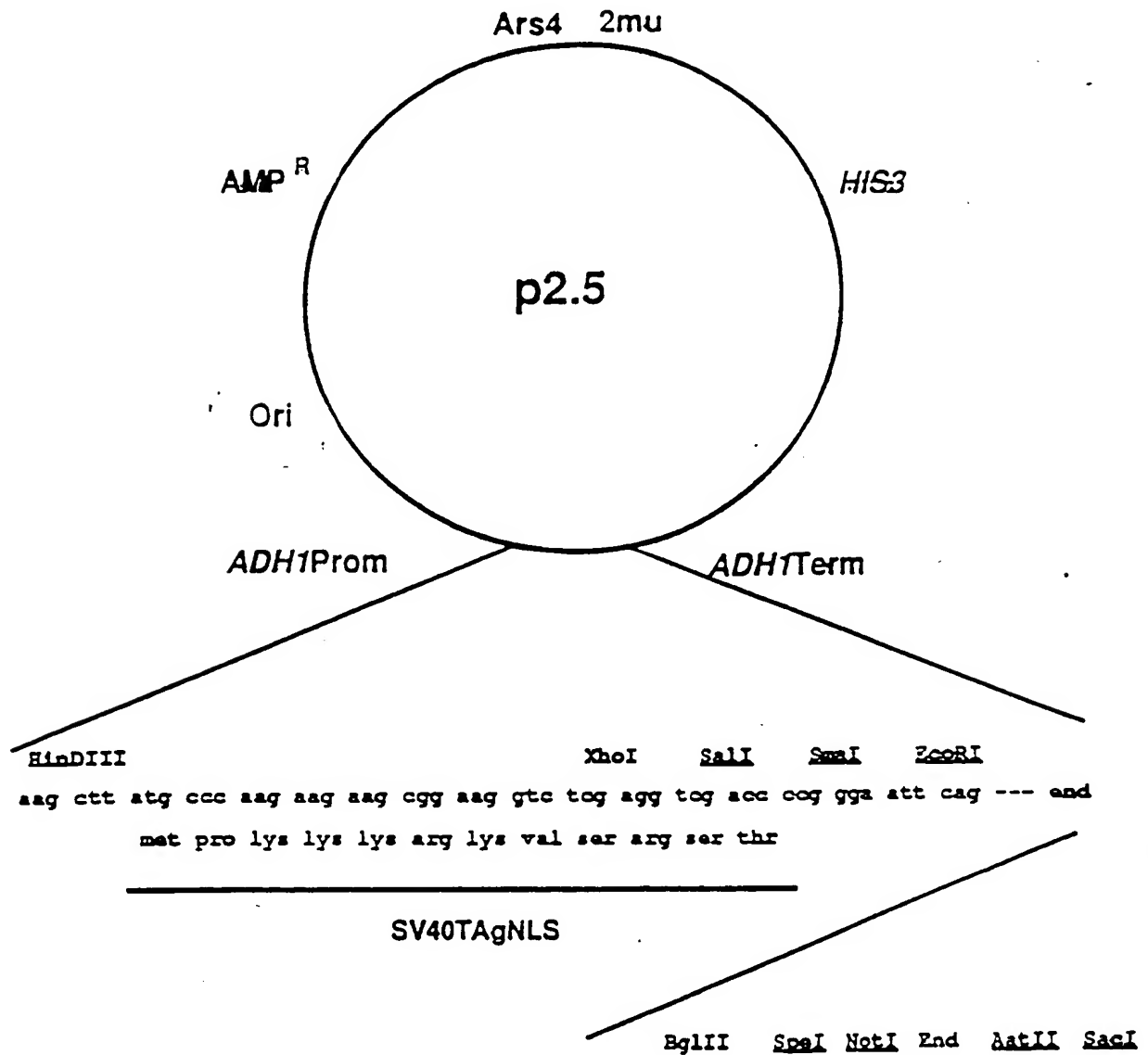


10027249-122101

FIGURE 2

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 REVERSE TWO-HYBRID SYSTEMS

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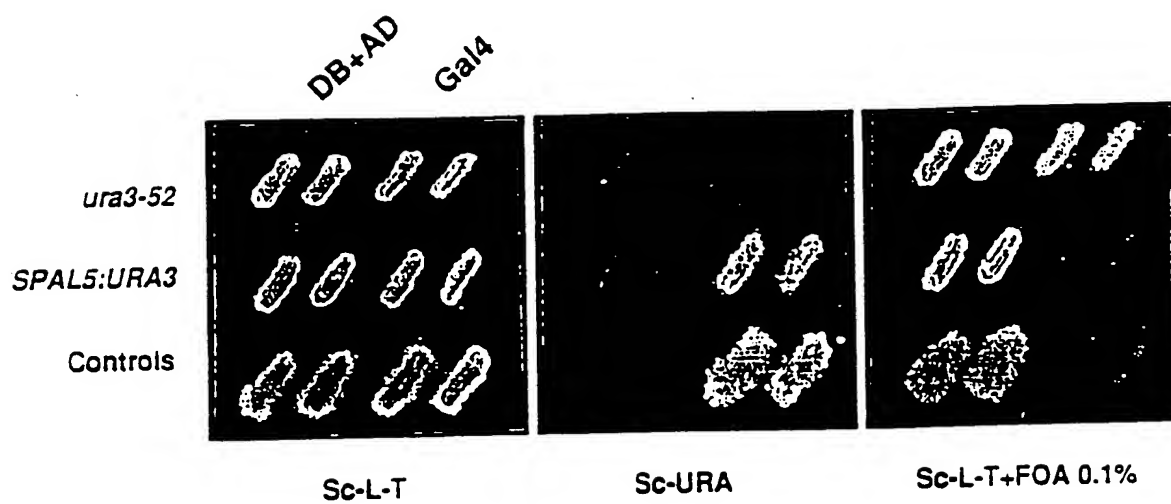


10027249-122101

FIGURE 3

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 Applicant(s): Marc Vidal et al.
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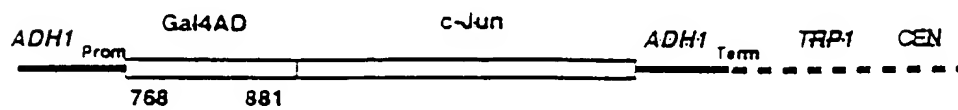
10027219-122101

[illegible]

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ADHI Prom Gal408D cFos ADHI Term LEU2 CEN

1 147



The schematic diagram shows a linear DNA construct. From left to right, it contains:
 - A thick black bar representing the **ADH1** promoter, labeled "Prom".
 - A box labeled **Gal4DBD** with an arrow pointing to a specific site.
 - A label **pRb** above the main line.
 - A solid line segment representing the **ADH1** coding sequence, starting at position **1** and ending at position **147**.
 - A dashed line segment representing the **ADH1** terminator, labeled "Term".
 - Two more dashed line segments labeled **LEU2** and **OEN**.

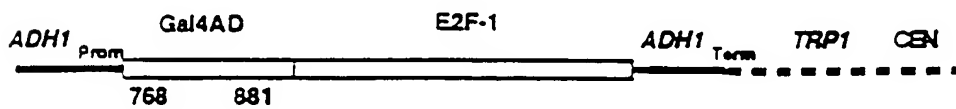
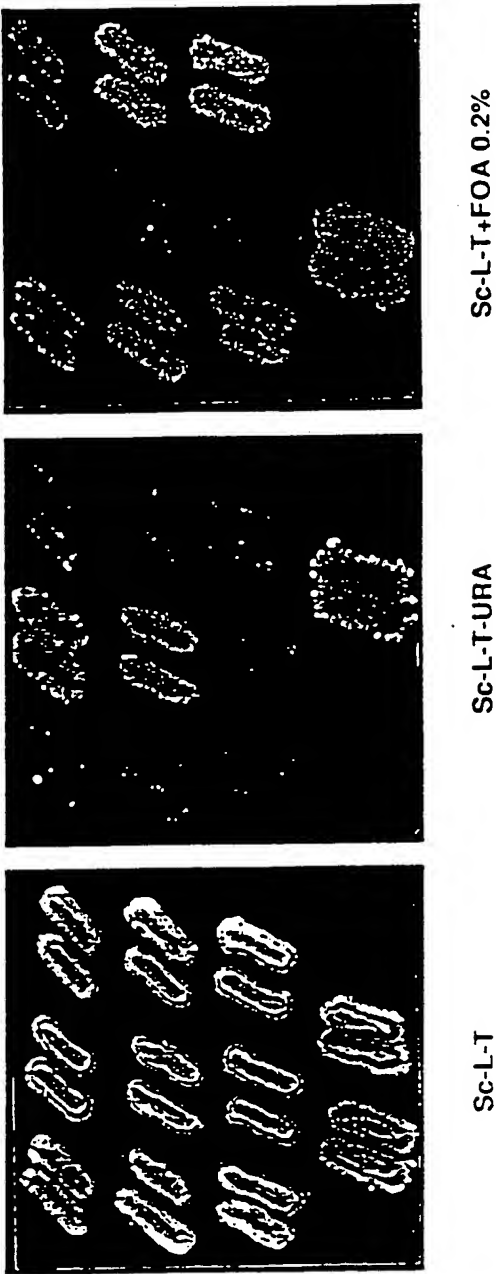


FIGURE 5

FOOTPRINT "5F2200T"



DB AD	Gal4	Vectors
DB-Fos AD	DB-Fos AD-Jun	DB AD-Jun
DB-Rb AD	DB-Rb AD-E2F	DB AD-E2F
Controls		

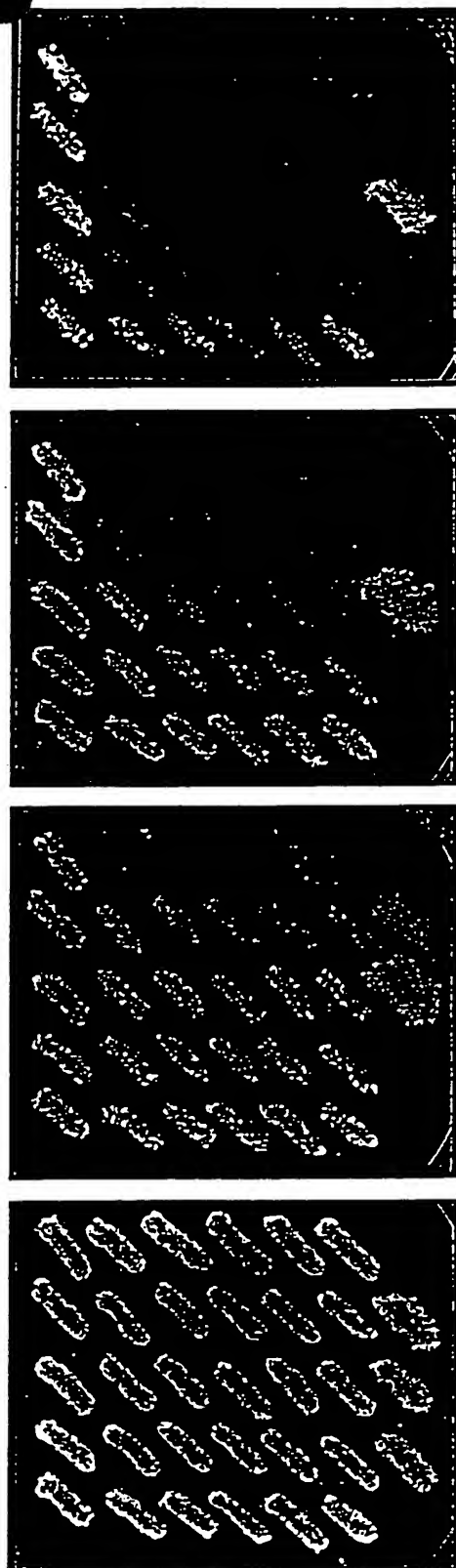
FIGURE 6

FOOTPRINT "572200T"

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DB+AD
DB-Jun+AD-Jun
DB-Rb+AD-E2F
DB-Fos+AD-Jun
Gal4



ura3-52
SPAL5:URA3
SPAL7:URA3
SPAL8:URA3
SPAL10:URA3
SPALX:URA3

Controls

Sc-L-T

Sc-L-T+FOA 0.05%

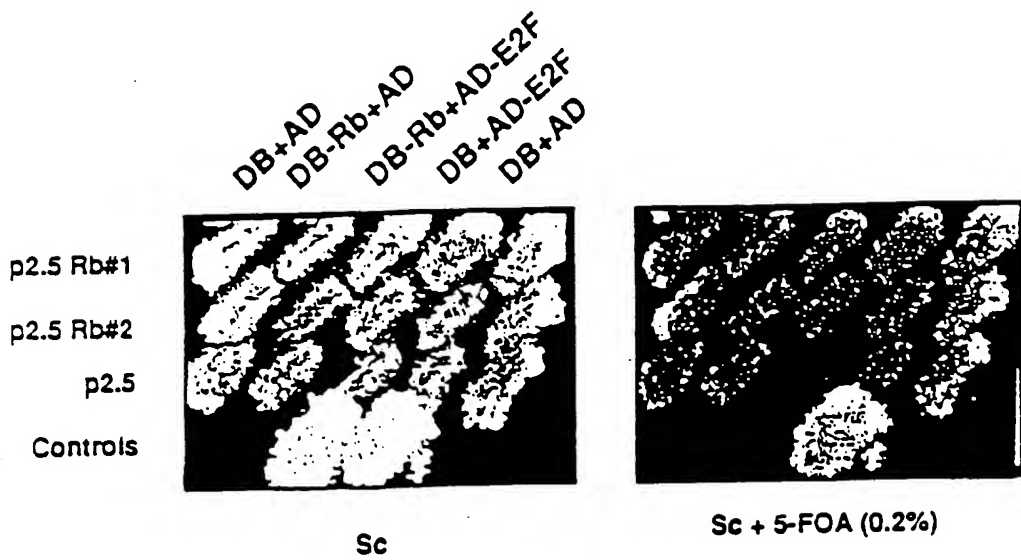
Sc-L-T+FOA 0.1%

Sc-L-T+FOA 0.2%



FIGURE 7

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REVERSE TWO-HYBRID SYSTEMS



FOOTNOTES

FOCAL STAINING

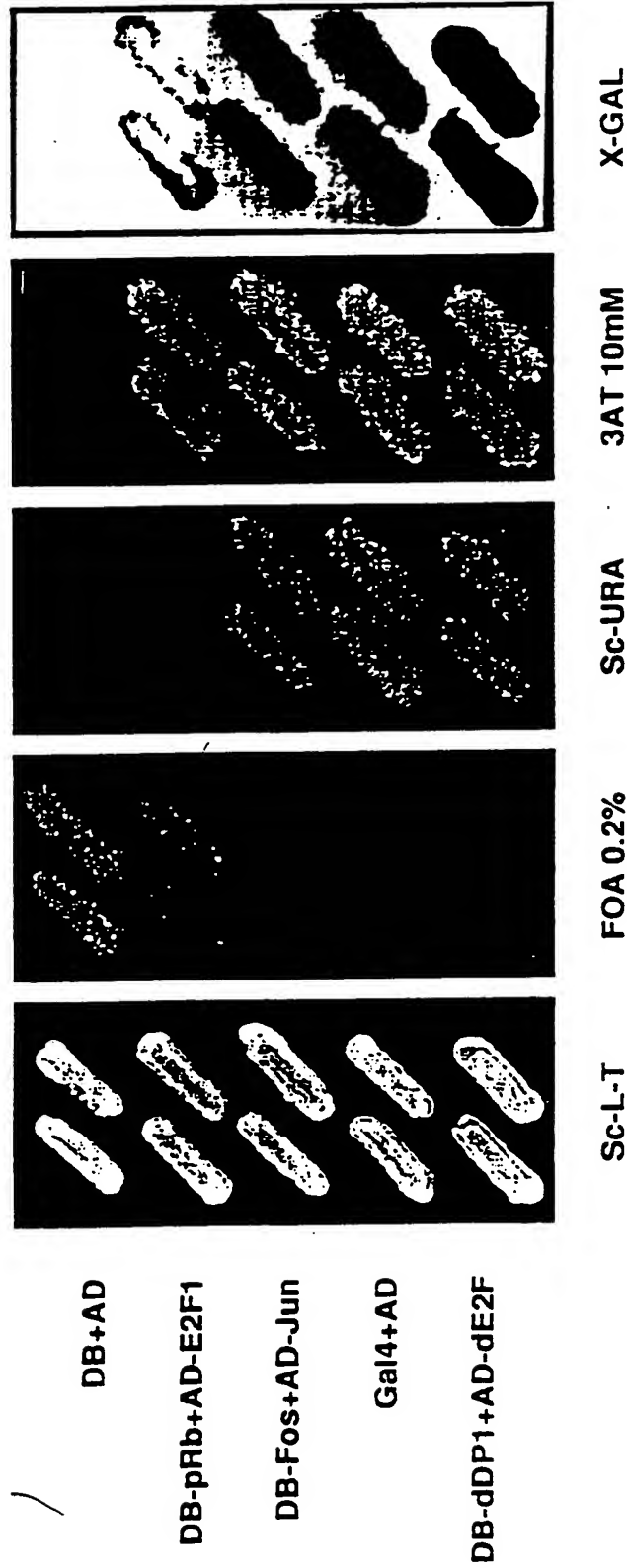
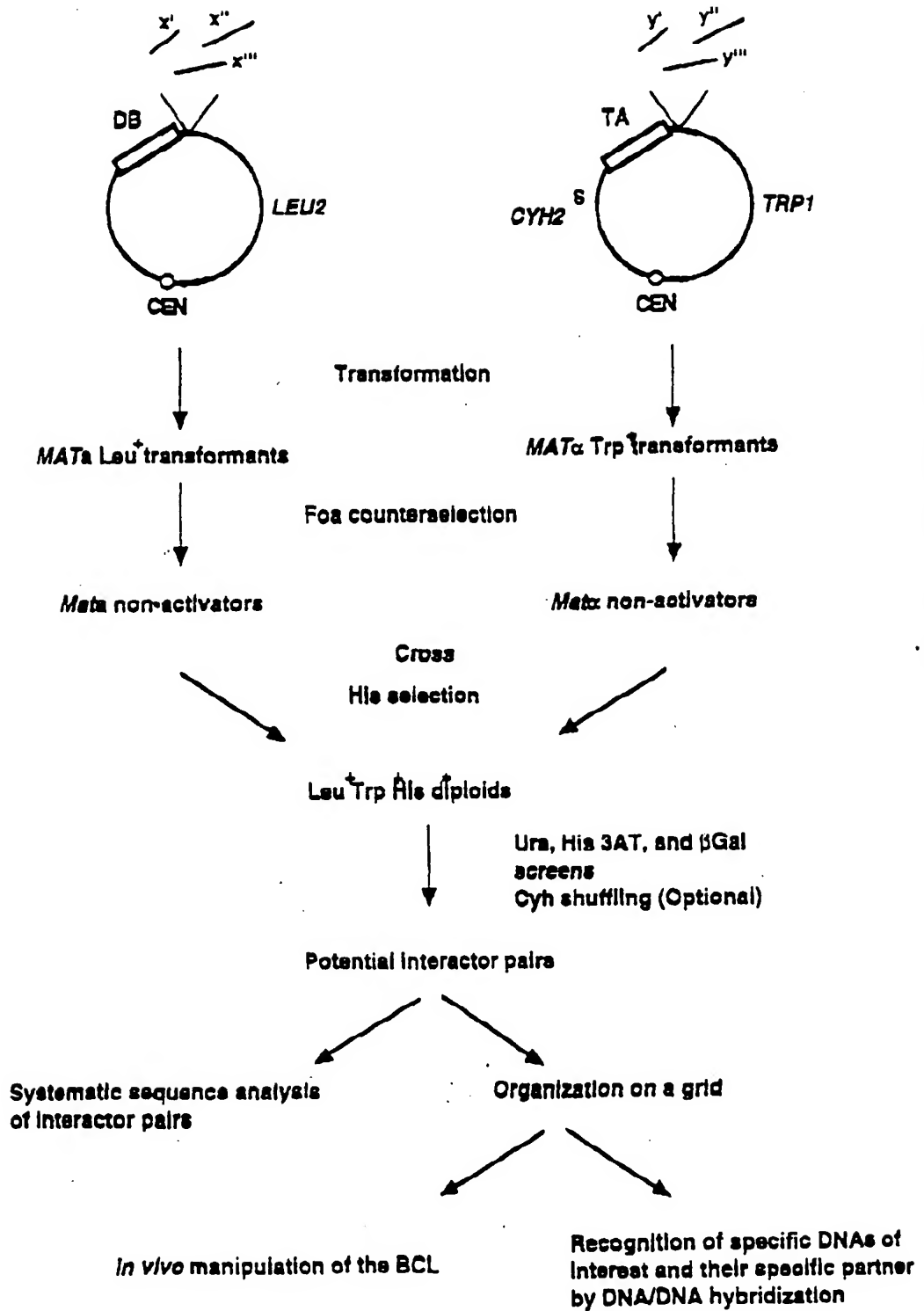


FIGURE 9



TOGETHER

GAL4
146 147

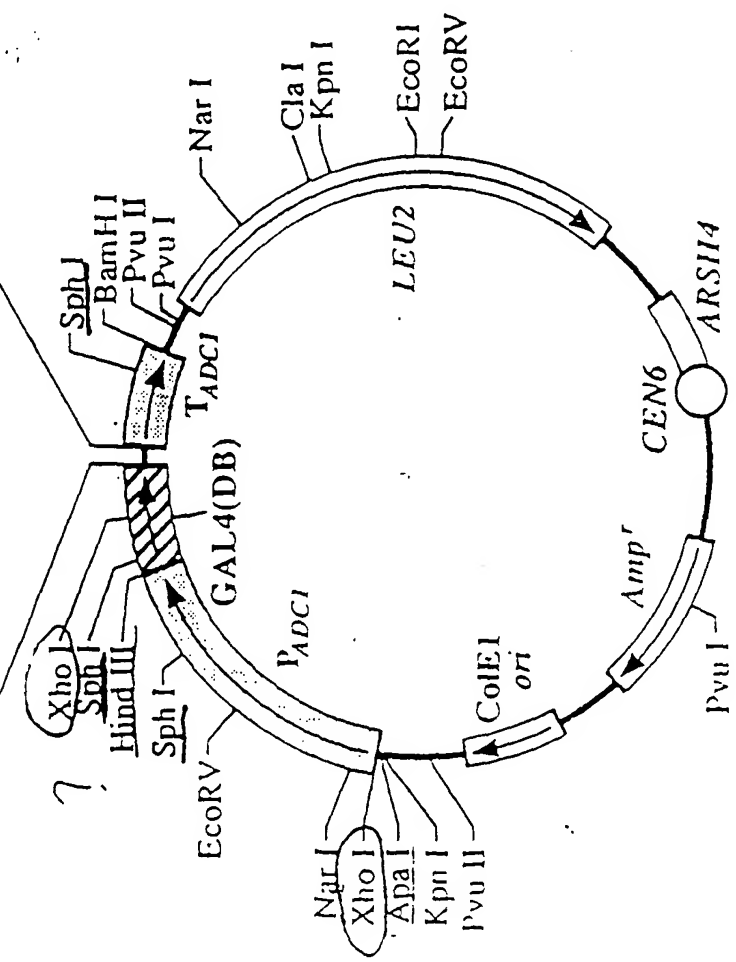
VAL SER SER ARG SER THR PRO GLY ILE GLN ILE TYR END
GTA TCG TCG AGG TCG ACC CCG GGA ATT CAG ATC TAC TAG TCGGGCCGC

Sal I Sma I EcoR I Bgl II Spe I Not I

END END END END END END
TAAGTAAGTAAGACGCTCTAAGTAAGTAAGCGCCGCCACCGCGGTGGAGCTTT

T_{ADCI}
Sac II

Aat II Sac I



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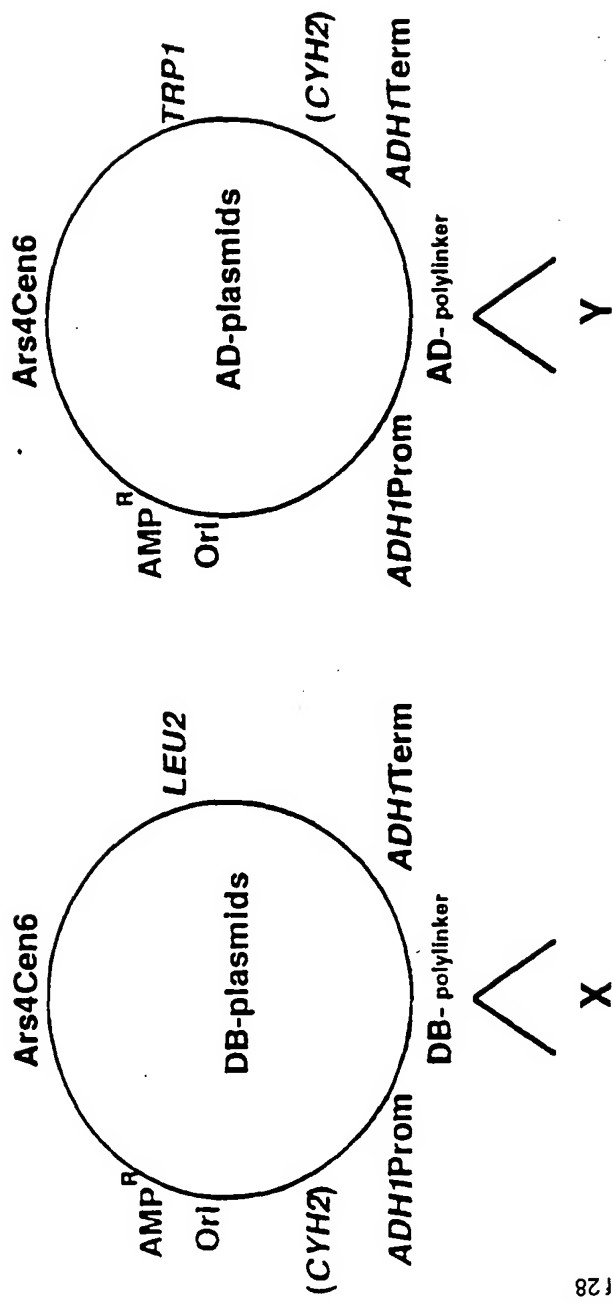
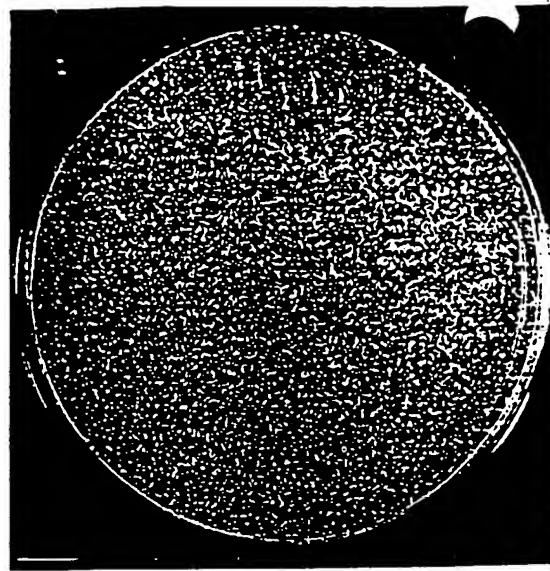


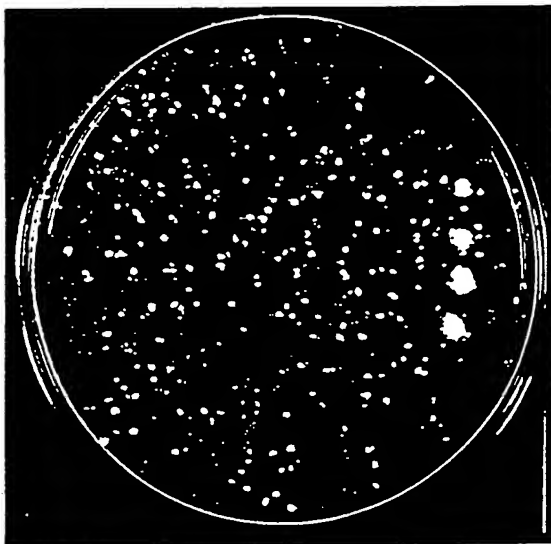
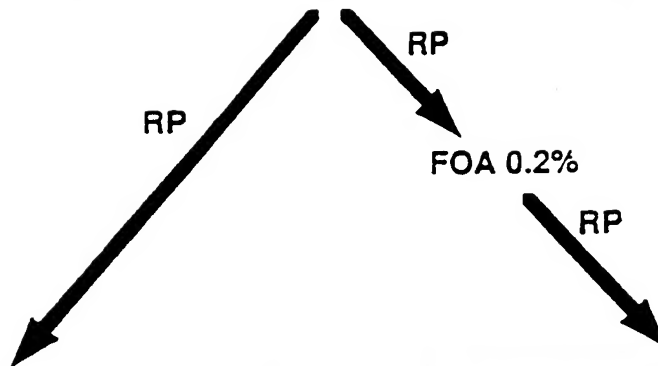
FIGURE 6

DB-X	Total	Hls+	Retested	Known Interacting	"Novel" Interacting	False positive
None	1x10 ⁶	1	0			
p130	5x10 ⁵	19	9	0	5 → 2	
DP1	2x10 ⁵	7	7	6 → 2	1 → 1	
pRb	1x10 ⁶	20	0			
p35	1x10 ⁶	20	8	0	8 → 2	0
CDK3	1x10 ⁶	38	16			
CDK3	1x10 ⁶	38	16			
DCC1	3x10 ⁶	81	23	0		
Zebu	1x10 ⁶	81	23			

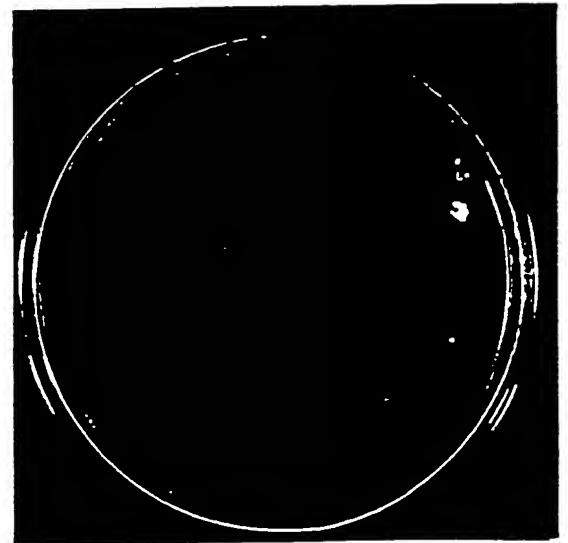
FIGURE 12



Sc-L



3AT 10mM



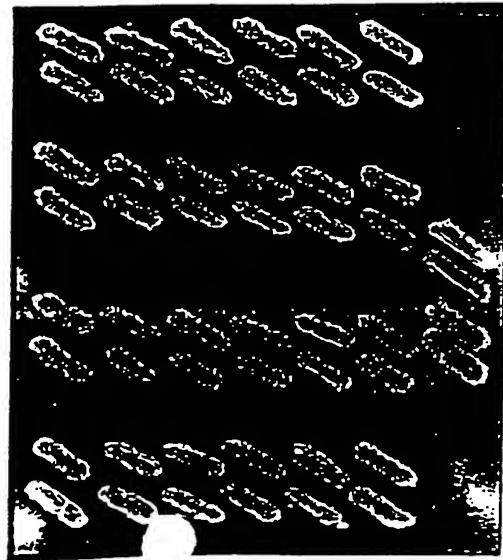
FOOTPRINT 672200T

DB-X	AD-Y	AD-pRb	AD-107	AD-130	DP1	CDK2	Jun	None
None								
E2F1		2	1					
E2F2		1	1					
E2F3					2			
E2F4								
Fos							24	
Jun								
CyclInA								
p21								
DCC1								39

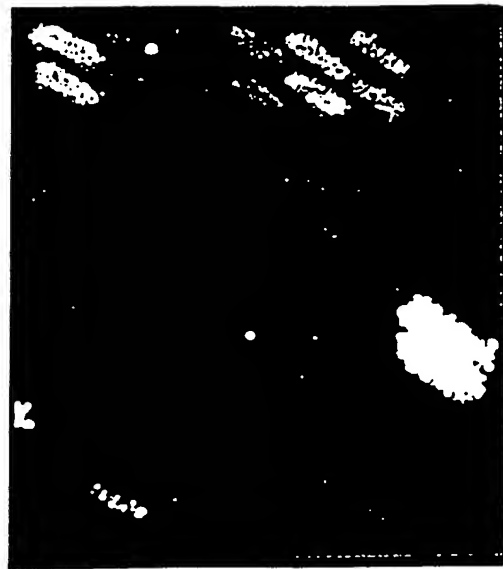
FIGURE 14

TECEP-5T2200T

DB-Rb + AD
DB-Rb + AD-E2F-1
DB-p107 + AD
DB-p107 + AD-E2F-4



Sc-L-T-H



Sc-L-T-H-U



Sc-L-T-H+FOA 0.2%

E1A#2
E1A#4
E1A-CR1
pRb
E1A-CR2
Controls

FIGURE 15

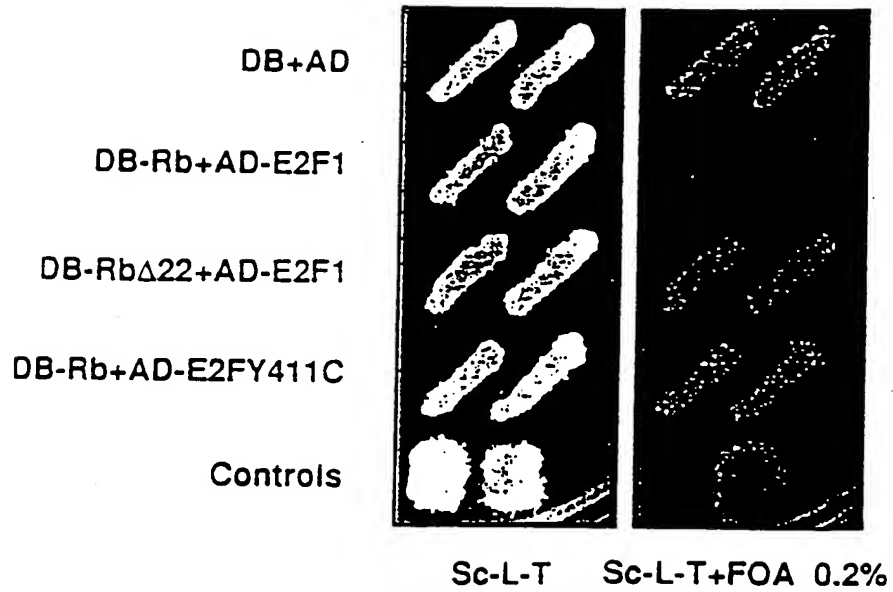
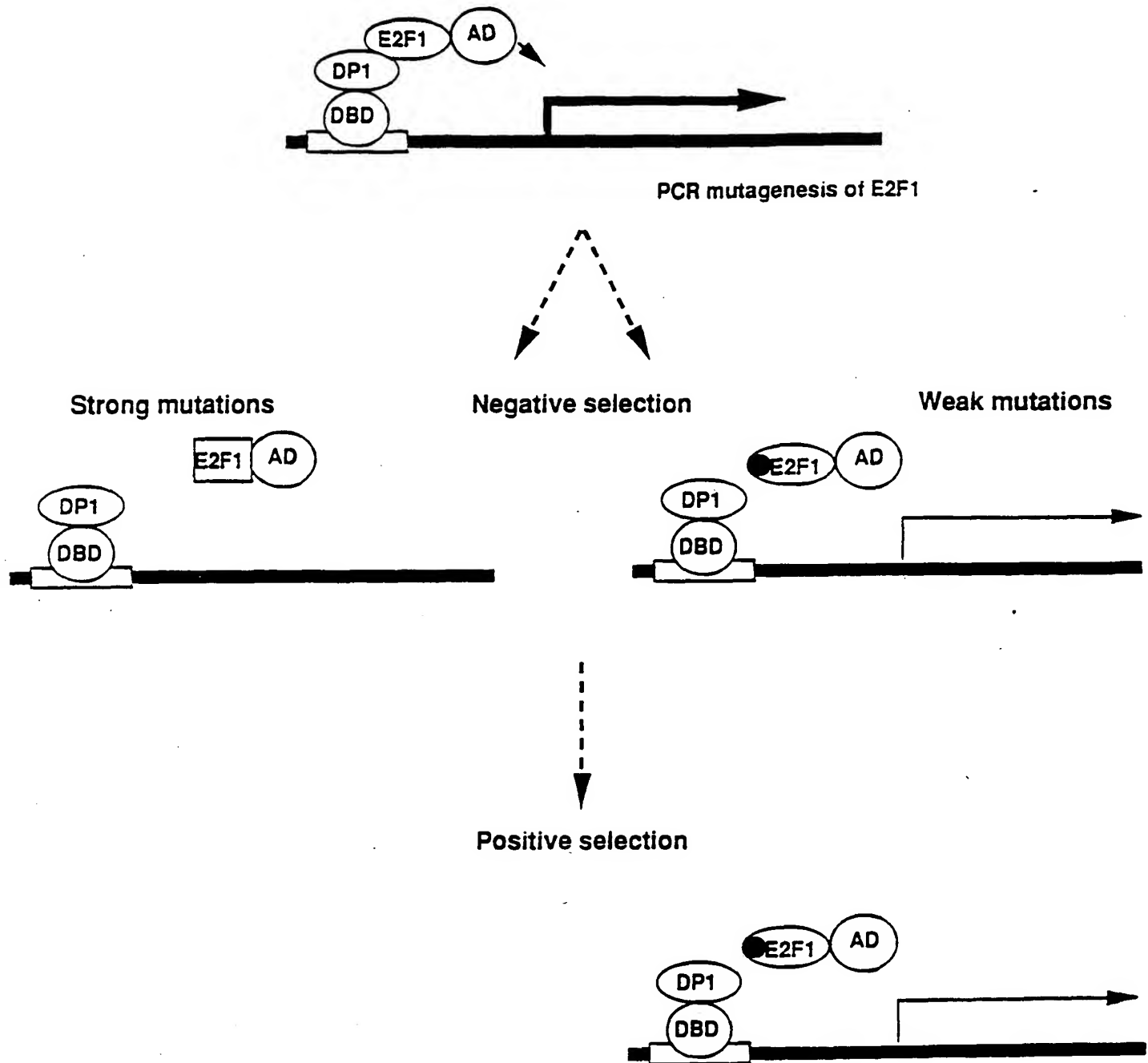


FIGURE 16



1002749-1204
FOI 2021-05122004

FIGURE 17
FOA⁺ SELECTION

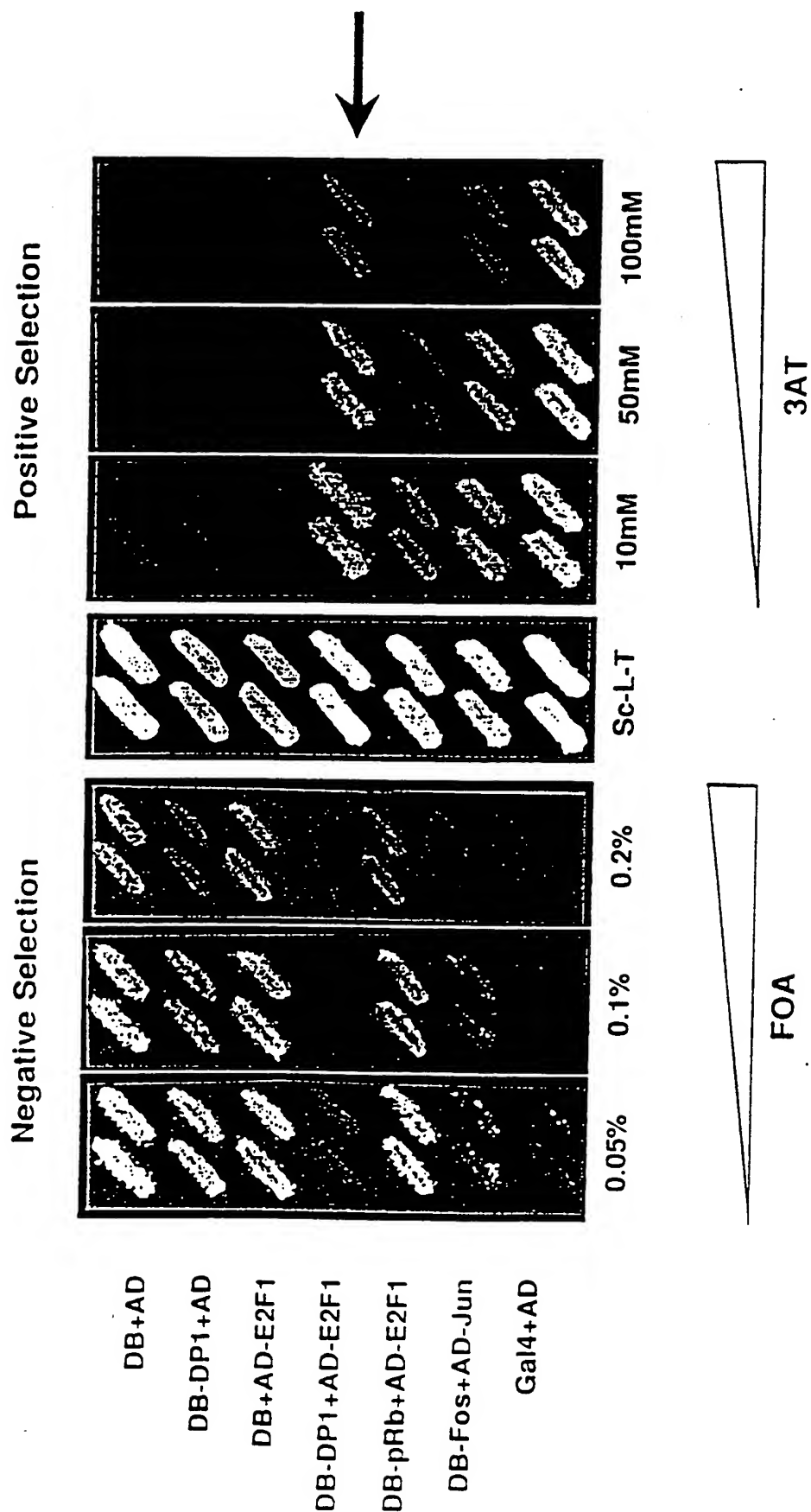
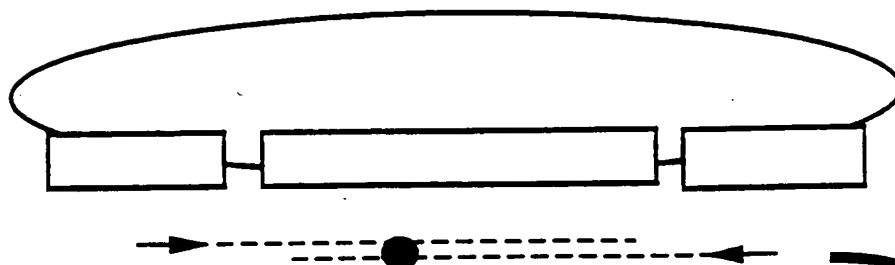


FIGURE 18A

PCR reaction



Gap repair

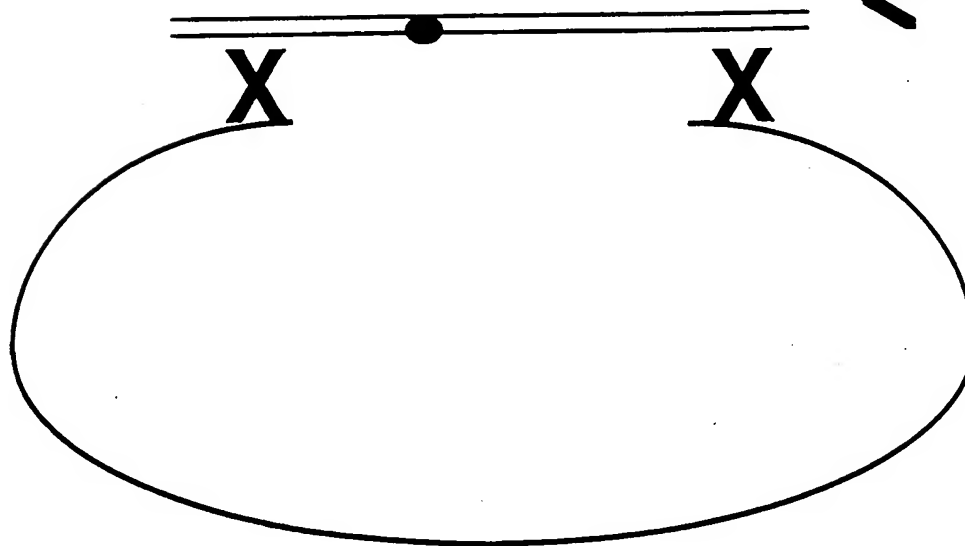
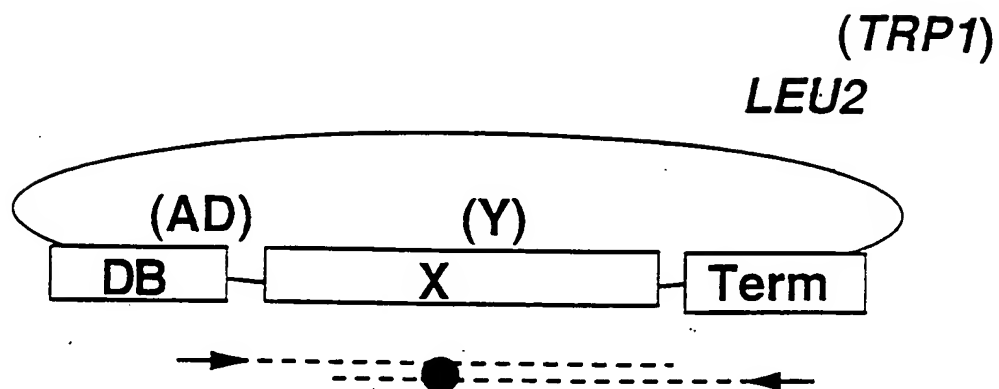


FIGURE 18A

In vitro mutagenic PCR reaction



In vivo gap repair

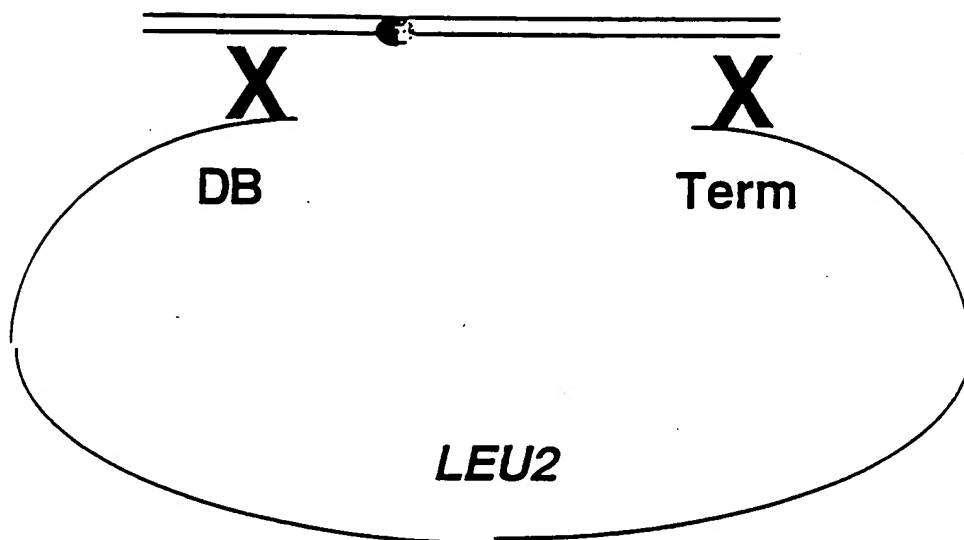


FIGURE 19

FOOTPRINT STADIUM

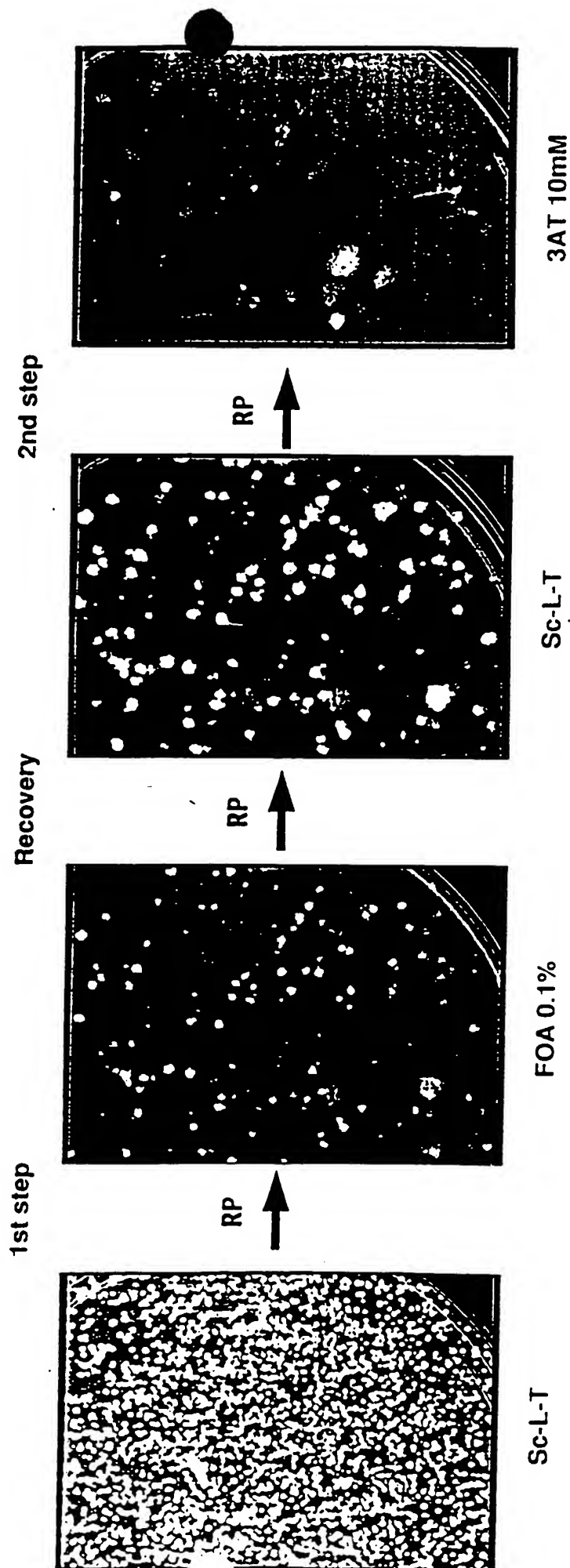


FIGURE 20

FOURTH STAGE

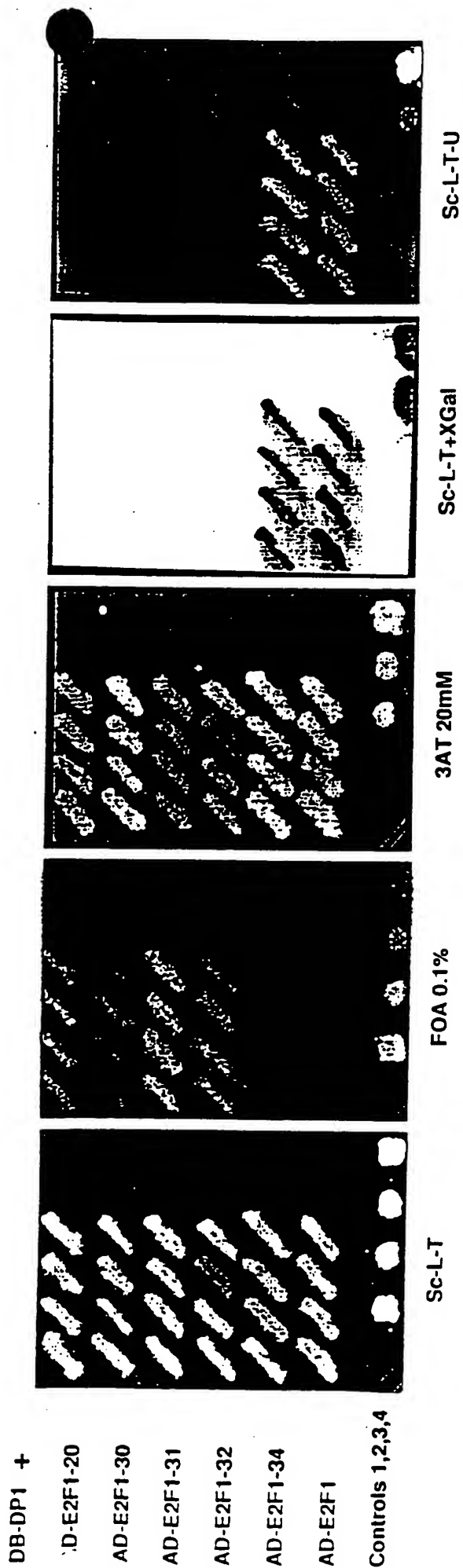


FIGURE 21

FOOTNOTES

MARKED BOX 2

283	Q	I	N	L	K	S	H	S	G	P	I	H	V	L	L	I	N	K	301	E2F5
	Q	I	H	L	K	S	V	S	G	P	I	E	V	L	L	V	N	K		E2F4
	Q	I	H	L	A	S	T	Q	G	P	I	E	V	Y	L	C	P	E		E2F3
	Q	I	Y	L	K	S	T	Q	G	P	I	E	V	Y	L	C	P	E		E2F2
	Q	I	S	L	K	S	K	Q	G	P	I	D	V	F	L	C	P	E		E2F1
T																				E2F1-20
																				E2F1-30
T																				E2F1-32
																				E2F1-31
N																				E2F1-65

FIGURE 22

TEF-221-672207

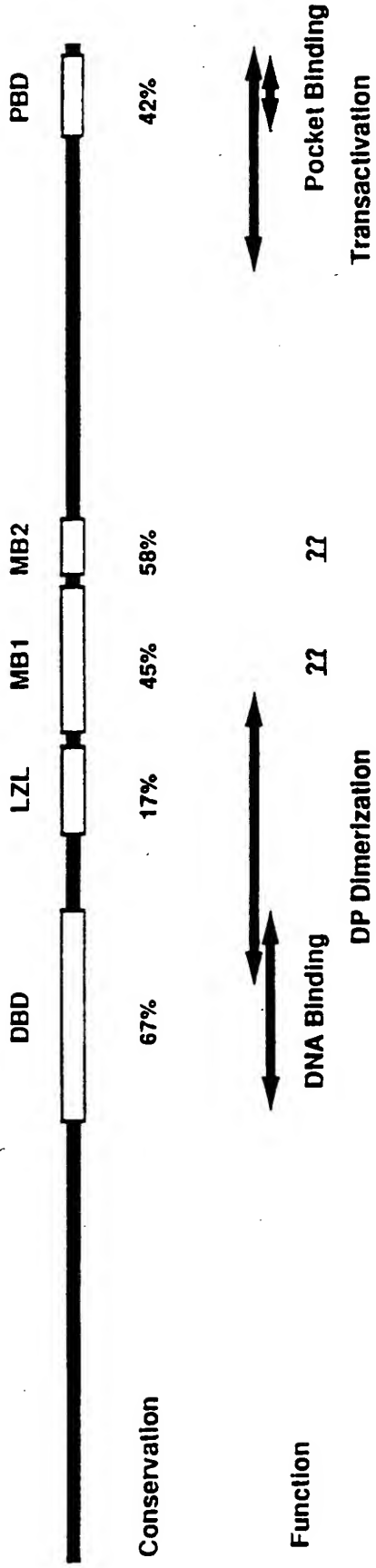


FIGURE 23A

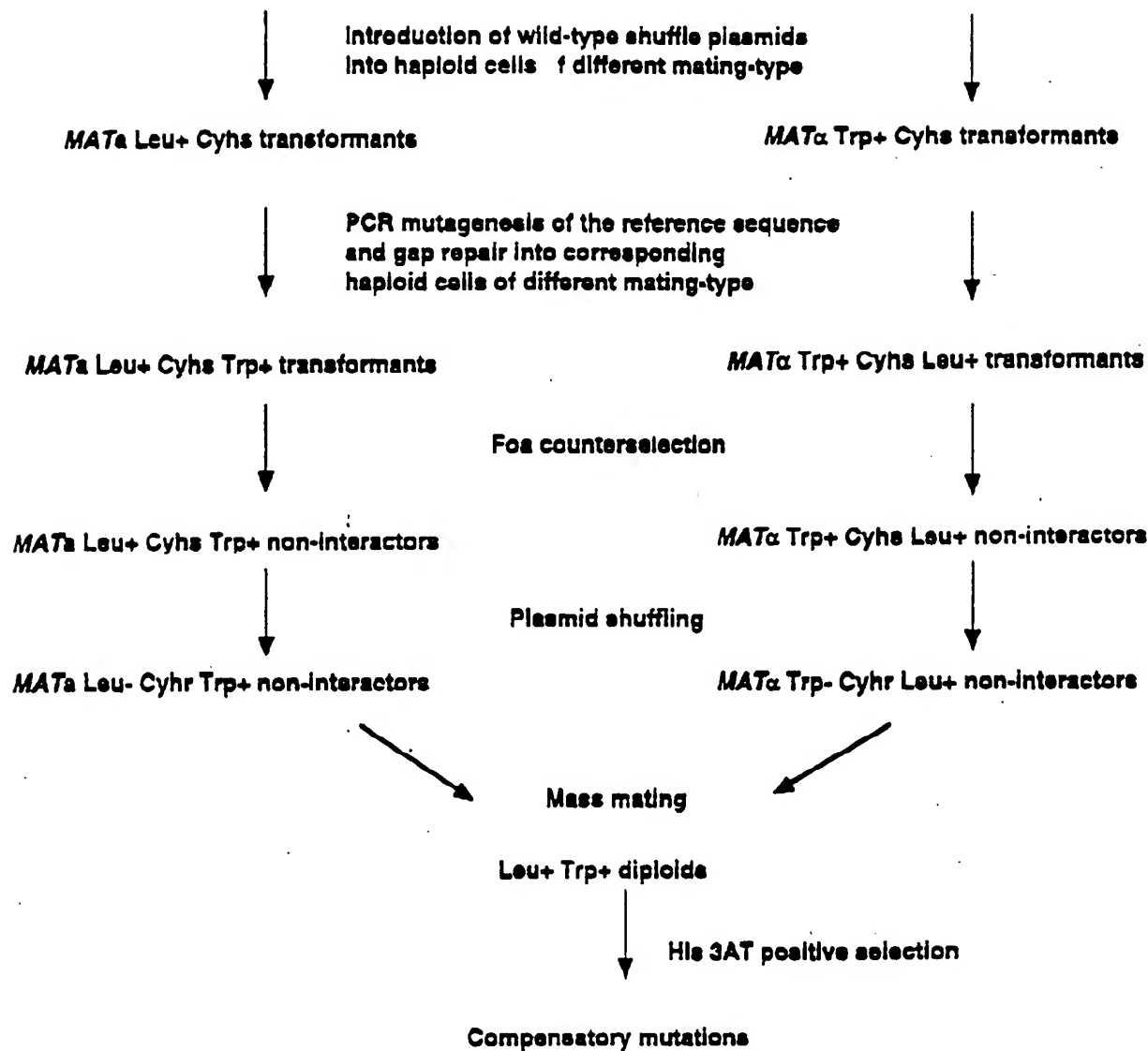


FIGURE 23B

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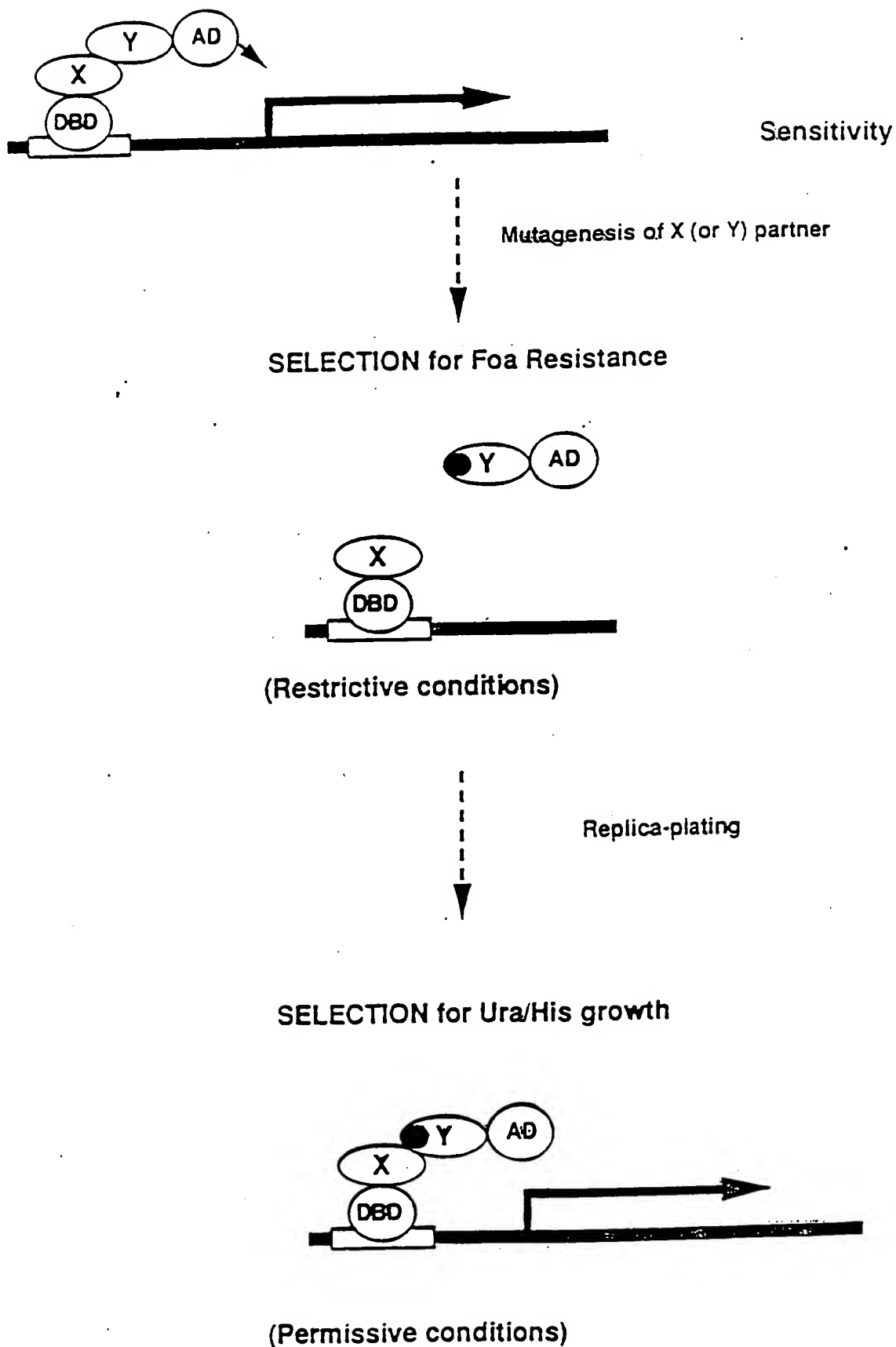


FIGURE 24

RECEIVED 5/22/00

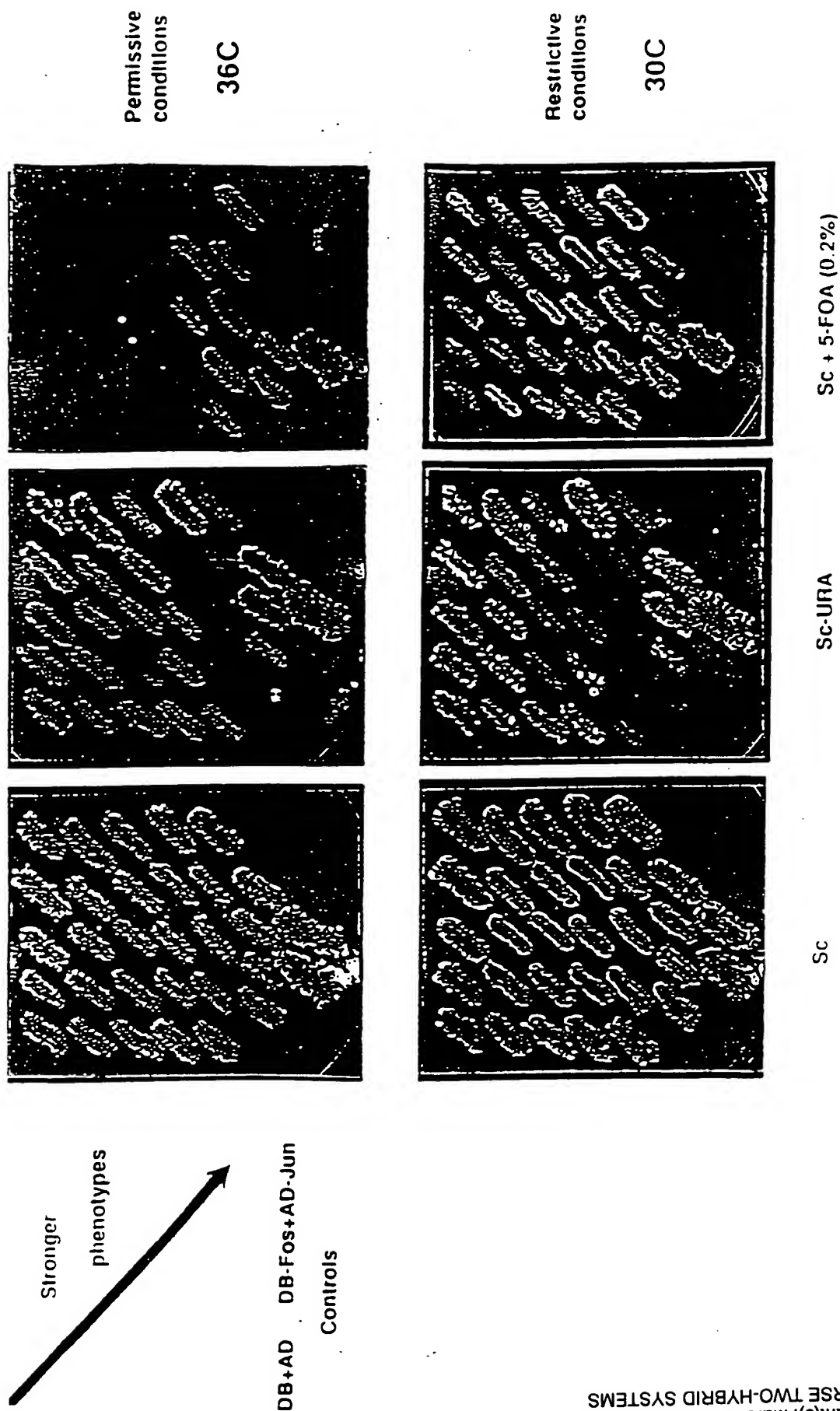


FIGURE 25

